



#5

SEQUENCE LISTING

<110> Farese, Robert V.
Cases, Sylvaine
Smith, Steven
Erickson, Sandra

<120> Diacylglycerol O-Acyltransferase

<130> UCAL-105CIP2

<140> 10/040,315
<141> 2001-10-29

<150> 60/107,771
<151> 1998-11-09

<150> PCT/US98/17883
<151> 1998-08-28

<150> 09/103,754
<151> 1998-06-24

<150> 09/339,472
<151> 1999-06-23

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<170> FastSEQ for Windows Version 3.0

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<213> homo sapiens

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 <212> DNA

<213> arabidopsis thaliana

<220>

<221> misc_feature

<222> (0)...(0)

<223> Each n residue at position 455, 464, 467, 475, 497, 500, 508, 514, 519, 536, 543, 544, 576, 583, 584 and 597 can be either a, c, g or t

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tttgaaaggc	gatcttctat	atgctattga	aagagtgttg	aagctttcag	ttccaaattt	180
atatgtgtgg	ctctgcatgt	tctactgctt	cttccacctt	tggtaaaca	tattggcaga	240
gcttctctgc	ttcggggatc	gtgaattcta	caaagattgg	tggaatgcaa	aaagtgtggg	300
agattactgg	gagaatgtgg	aatatgcctg	tccataaatg	ggatgggtcc	gacatatata	360
ccttccccgt	gcttgccgac	aaggattacc	caaagacacc	ccggccatta	accattggct	420
ttcccaagcc	ccctggaggc	ctttccatgg	gccanggacc	cgnggtnc	tggnngccc	480
ttcaaagcaa	aggggnttn	cctggggnta	aagntccang	ggcccttggg	gcccanc	540
aannttcccc	cgggaaagg	tgcccaccg	ggggngaaa	aannccggg	ggcaccncg	600
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<210> 5

<211> 386

<212> PRT

<213> homo sapiens

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Cys	Leu	Val	Ile	Ala	Ala	Asn	Val	Phe	Ala	Val	Ala	Ala	Phe	Gln	Val
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Glu	Lys	Arg	Leu	Ala	Val	Gly	Ala	Leu	Thr	Glu	Gln	Ala	Gly	Leu	Leu
	50					55					60				
Leu	His	Val	Ala	Asn	Leu	Ala	Thr	Ile	Leu	Cys	Phe	Pro	Ala	Ala	Val
	65				70					75					80
Val	Leu	Leu	Val	Glu	Ser	Ile	Thr	Pro	Val	Gly	Ser	Leu	Leu	Ala	Leu
				85					90					95	
Met	Ala	His	Thr	Ile	Leu	Phe	Leu	Lys	Leu	Phe	Ser	Tyr	Arg	Asp	Val
			100					105					110		
Asn	Ser	Trp	Cys	Arg	Arg	Ala	Arg	Ala	Lys	Ala	Ala	Ser	Ala	Gly	Lys
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Lys	Ala	Ser	Ser	Val	Ala	Ala	Pro	His	Thr	Val	Ser	Tyr	Pro	Asp	Asn
	130					135					140				
Leu	Thr	Tyr	Arg	Asp	Leu	Tyr	Tyr	Phe	Leu	Phe	Ala	Pro	Thr	Leu	Cys
	145				150				155						160
Tyr	Glu	Leu	Asn	Phe	Pro	Arg	Ser	Pro	Arg	Ile	Arg	Lys	Arg	Phe	Leu
			165						170					175	
Leu	Arg	Arg	Ile	Leu	Glu	Met	Leu	Phe	Phe	Thr	Gln	Leu	Gln	Val	Gly
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Leu	Ile	Gln	Trp	Met	Val	Pro	Thr	Ile	Gln	Asn	Ser	Met	Lys	Pro	
		195				200					205				
Phe	Lys	Asp	Met	Asp	Tyr	Ser	Arg	Ile	Ile	Glu	Arg	Leu	Leu	Lys	Leu
	210					215				220					
Ala	Val	Pro	Asn	His	Leu	Ile	Trp	Leu	Ile	Phe	Phe	Tyr	Trp	Leu	Phe
	225				230					235					240

His Ser Cys Leu Asn Ala Val Ala Glu Leu Met Gln Phe Gly Asp Arg
 245 250 255
 Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu Ser Val Thr Tyr Phe Trp
 260 265 270
 Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe Tyr
 275 280 285
 Lys Pro Met Leu Arg Arg Gly Ser Ser Lys Trp Met Ala Arg Thr Gly
 290 295 300
 Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val Ser Val Pro
 305 310 315 320
 Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Gly Met Met Ala Gln Ile
 325 330 335
 Pro Leu Ala Trp Phe Val Gly Arg Phe Phe Gln Gly Asn Tyr Gly Asn
 340 345 350
 Ala Ala Val Trp Leu Ser Leu Ile Ile Gly Gln Pro Ile Ala Val Leu
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 Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Glu Ala Pro Ala Ala
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 Glu Ala
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<210> 6
 <211> 488
 <212> PRT
 <213> homo sapiens

<400> 6
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 35 40 45
 Pro Ala Pro Asn Lys Asp Gly Asp Ala Gly Val Gly Ser Gly His Trp
 50 55 60
 Glu Leu Arg Cys His Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser
 65 70 75 80
 Gly Phe Ser Asn Tyr Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu
 85 90 95
 Ile Leu Ser Asn Ala Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly
 100 105 110
 Ile Leu Val Asp Pro Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro
 115 120 125
 His Ser Trp Pro Ala Pro Cys Leu Val Ile Ala Ala Asn Val Phe Ala
 130 135 140
 Val Ala Ala Phe Gln Val Glu Lys Arg Leu Ala Val Gly Ala Leu Thr
 145 150 155 160
 Glu Gln Ala Gly Leu Leu Leu His Val Ala Asn Leu Ala Thr Ile Leu
 165 170 175
 Cys Phe Pro Ala Ala Val Val Leu Leu Val Glu Ser Ile Thr Pro Val
 180 185 190
 Gly Ser Leu Ala Leu Met Ala His Thr Ile Leu Phe Leu Lys Leu
 195 200 205
 Phe Ser Tyr Arg Asp Val Asn Ser Trp Cys Arg Arg Ala Arg Ala Lys
 210 215 220
 Ala Ala Ser Ala Gly Lys Lys Ala Ser Ser Ala Ala Ala Pro His Thr
 225 230 235 240

Val Ser Tyr Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Leu
 245 250 255
 Phe Ala Pro Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg
 260 265 270
 Ile Arg Lys Arg Phe Leu Leu Arg Arg Ile Leu Glu Met Leu Phe Phe
 275 280 285
 Thr Gln Leu Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile
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 Gln Asn Ser Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile
 305 310 315 320
 Glu Arg Leu Leu Lys Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile
 325 330 335
 Phe Phe Tyr Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu
 340 345 350
 Met Gln Phe Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ser Glu
 355 360 365
 Ser Val Thr Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp
 370 375 380
 Cys Ile Arg His Phe Tyr Lys Pro Met Leu Arg Arg Gly Ser Ser Lys
 385 390 395 400
 Trp Met Ala Arg Thr Gly Val Phe Leu Ala Ser Ala Phe Phe His Glu
 405 410 415
 Tyr Leu Val Ser Val Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr
 420 425 430
 Gly Met Met Ala Gln Ile Pro Leu Ala Trp Phe Val Gly Arg Phe Phe
 435 440 445
 Gln Gly Asn Tyr Gly Asn Ala Ala Val Trp Leu Ser Leu Ile Ile Gly
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 <211> 498
 <212> PRT
 <213> mus musculus

<400> 7
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 35 40 45
 Ala Pro Ala Pro Ala Pro Ala Pro Ala His Thr Arg Asp Lys Asp Gly
 50 55 60
 Arg Thr Ser Val Gly Asp Gly Tyr Trp Asp Leu Arg Cys His Arg Leu
 65 70 75 80
 Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr Arg Gly
 85 90 95
 Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala Arg Leu
 100 105 110
 Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro Ile Gln
 115 120 125
 Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala Pro Cys
 130 135 140

Val	Ile	Ile	Ala	Ser	Asn	Ile	Phe	Val	Val	Ala	Ala	Phe	Gln	Ile	Glu
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Lys	Arg	Leu	Ala	Val	Gly	Ala	Leu	Thr	Glu	Gln	Met	Gly	Leu	Leu	Leu
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His	Val	Val	Asn	Leu	Ala	Thr	Ile	Ile	Cys	Phe	Pro	Ala	Ala	Val	Ala
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Leu	Leu	Val	Glu	Ser	Ile	Thr	Pro	Val	Gly	Ser	Val	Phe	Ala	Leu	Ala
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Ser	Tyr	Ser	Ile	Met	Phe	Leu	Lys	Leu	Tyr	Ser	Tyr	Arg	Asp	Val	Asn
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Leu	Trp	Cys	Arg	Gln	Arg	Arg	Val	Lys	Ala	Lys	Ala	Val	Ser	Thr	Gly
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Lys	Lys	Val	Ser	Gly	Ala	Ala	Ala	Gln	Gln	Ala	Val	Ser	Tyr	Pro	Asp
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Asn	Leu	Thr	Tyr	Arg	Asp	Leu	Tyr	Tyr	Phe	Ile	Phe	Ala	Pro	Thr	Leu
			260					265					270		
Cys	Tyr	Glu	Leu	Asn	Phe	Pro	Arg	Ser	Pro	Arg	Ile	Arg	Lys	Arg	Phe
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Leu	Leu	Arg	Arg	Val	Leu	Glu	Met	Leu	Phe	Phe	Thr	Gln	Leu	Gln	Val
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Gly	Leu	Ile	Gln	Gln	Trp	Met	Val	Pro	Thr	Ile	His	Asn	Ser	Met	Lys
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Pro	Phe	Lys	Asp	Met	Asp	Tyr	Ser	Arg	Ile	Ile	Glu	Arg	Leu	Leu	Lys
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Leu	Ala	Val	Pro	Asn	His	Leu	Ile	Trp	Leu	Ile	Phe	Phe	Tyr	Trp	Phe
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Phe	His	Ser	Cys	Leu	Asn	Ala	Val	Ala	Glu	Leu	Leu	Gln	Phe	Gly	Asp
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Arg	Glu	Phe	Tyr	Arg	Asp	Trp	Trp	Asn	Ala	Glu	Ser	Val	Thr	Tyr	Phe
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Trp	Gln	Asn	Trp	Asn	Ile	Pro	Val	His	Lys	Trp	Cys	Ile	Arg	His	Phe
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Tyr	Lys	Pro	Met	Leu	Arg	His	Gly	Ser	Ser	Lys	Trp	Val	Ala	Arg	Thr
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Gly	Val	Phe	Leu	Thr	Ser	Ala	Phe	Phe	His	Glu	Tyr	Leu	Val	Ser	Val
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Pro	Leu	Arg	Met	Phe	Arg	Leu	Trp	Ala	Phe	Thr	Ala	Met	Met	Ala	Gln
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Val	Pro	Leu	Ala	Trp	Ile	Val	Gly	Arg	Phe	Phe	Gln	Gly	Asn	Tyr	Gly
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Gly Val

<210> 8
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic peptide-FLAG epitope

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<210> 9

<211> 1650

<212> DNA

<213> mus musculus

<400> 9

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<210> 10

<211> 498

<212> PRT

<213> mus musculus

<400> 10

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			20					25					30		
Glu	Val	Arg	Asp	Ala	Ala	Val	Ser	Pro	Asp	Leu	Gly	Ala	Gly	Gly	Asp
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Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	His	Thr	Arg	Asp	Lys	Asp	Gly
			50				55			60					
Arg	Thr	Ser	Val	Gly	Asp	Gly	Tyr	Trp	Asp	Leu	Arg	Cys	His	Arg	Leu
65					70				75					80	
Gln	Asp	Ser	Leu	Phe	Ser	Ser	Asp	Ser	Gly	Phe	Ser	Asn	Tyr	Arg	Gly
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Ile	Leu	Asn	Trp	Cys	Val	Val	Met	Leu	Ile	Leu	Ser	Asn	Ala	Arg	Leu
			100					105					110		

Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro Ile Gln
115 120 125
Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala Pro Cys
130 135 140
Val Ile Ile Ala Ser Asn Ile Phe Val Val Ala Ala Phe Gln Ile Glu
145 150 155 160
Lys Arg Leu Ala Val Gly Ala Leu Thr Glu Gln Met Gly Leu Leu Leu
165 170 175
His Val Val Asn Leu Ala Thr Ile Ile Cys Phe Pro Ala Ala Val Ala
180 185 190
Leu Leu Val Glu Ser Ile Thr Pro Val Gly Ser Val Phe Ala Leu Ala
195 200 205
Ser Tyr Ser Ile Met Phe Leu Lys Leu Tyr Ser Tyr Arg Asp Val Asn
210 215 220
Leu Trp Cys Arg Gln Arg Arg Val Lys Ala Lys Ala Val Ser Thr Gly
225 230 235 240
Lys Lys Val Ser Gly Ala Ala Ala Gln Gln Ala Val Ser Tyr Pro Asp
245 250 255
Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Ile Phe Ala Pro Thr Leu
260 265 270
Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys Arg Phe
275 280 285
Leu Leu Arg Arg Val Leu Glu Met Leu Phe Phe Thr Gln Leu Gln Val
290 295 300
Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile His Asn Ser Met Lys
305 310 315 320
Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu Leu Lys
325 330 335
Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr Trp Phe
340 345 350
Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Leu Gln Phe Gly Asp
355 360 365
Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ala Glu Ser Val Thr Tyr Phe
370 375 380
Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg His Phe
385 390 395 400
Tyr Lys Pro Met Leu Arg His Gly Ser Ser Lys Trp Val Ala Arg Thr
405 410 415
Gly Val Phe Leu Thr Ser Ala Phe Phe His Glu Tyr Leu Val Ser Val
420 425 430
Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Ala Met Met Ala Gln
435 440 445
Val Pro Leu Ala Trp Ile Val Gly Arg Phe Phe Gln Gly Asn Tyr Gly
450 455 460
Asn Ala Ala Val Trp Val Thr Leu Ile Ile Gly Gln Pro Val Ala Val
465 470 475 480
Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Asp Ala Pro Val
485 490 495
Gly Val